

### **Amendments to the Claims:**

The following list of claims will replace all prior versions of the claims in the application:

1. (*Currently amended*) A method of managing and retrieving biological data for efficient exploration and analysis, the method comprising:

acquiring and staging gene expression data for storage, wherein the gene expression data comprises hybridization experiment data from microarray samples prepared from tissues and cell lines;

providing storing the gene expression data in a data warehouse which comprises comprising three distinct databases comprising a gene expression database for storing quantitative gene expression measurements for the tissues and cell lines[[]], a clinical database for storing sample data on bio-samples and donors ~~corresponding to~~ from which the tissues and cell lines were obtained[[]], and a fragment index database for storing information on biological properties and gene sequences for DNA fragments ~~corresponding to the tissues and cell lines in~~ microarrays from which the gene expression measurements were obtained, wherein the data warehouse is arranged in a relational format, and wherein staging comprises linking gene expression measurements in the gene expression database with sample data in the clinical database and information in the fragment index database;

providing a user interface for entry of a first query, wherein the first query comprises a first sample set or gene set for which additional information is sought, and wherein the sample set comprises a plurality of samples having one or more selected attributes and the gene set comprises at least one gene having one or more selected properties;

receiving the first query;

correlating gene expression measurements within the gene expression database with the first sample set or gene set of the first query; and

displaying at the user interface the correlated gene expression measurements that are responsive to the first query.

2. (*Original*) The method of claim 1, wherein the data warehouse is constructed in a star relational schema.

3. (*Original*) The method of claim 1, wherein the data warehouse is constructed in a snowflake relational schema.

4. (*Currently amended*) The method of claim 1, ~~wherein the analysis comprises further comprising~~ a gene signature analysis ~~and the method further that~~ comprises analyzing the correlated gene expression measurements to identify a present set of DNA fragments that are ~~consistently expressed~~ present within the first sample set or gene set, and an absent set of DNA fragments that are ~~consistently not expressed~~ absent within the first sample set or gene set.

5. (*Currently amended*) The method of claim 4, ~~wherein the analysis comprises further comprising~~ a gene signature differential analysis ~~and the method further comprises that~~ comprises:

performing a gene signature analysis for a second sample set or gene set;  
comparing the two different gene signature analysis results; and  
identifying four sets of DNA gene fragments comprising:

a present/absent gene set including fragments that are ~~consistently expressed~~ present within the first sample set or gene set and ~~consistently not expressed~~ absent within the second sample set or gene set;

a present/present gene set including fragments that are ~~consistently expressed~~ present within both the first and second sample set or gene set;

an absent/absent gene set including fragments that are ~~consistently not expressed~~ absent within both the first and second sample set or gene set; and

an absent/present gene set including fragments that are ~~consistently not expressed~~ absent within the first sample set or gene set and are ~~consistently expressed~~ present within the second sample set or gene set.

6. (*Currently amended*) The method of claim 1, ~~wherein the analysis comprises further comprising~~ a fold change analysis ~~comprising that comprises:~~

calculating mean expression levels for each gene fragment within the first sample set or gene set;

before or after calculating mean expression levels for the first sample set or gene set, correlating gene expression measurements with a second query comprising a second sample set or gene set;

calculating mean expression levels of each gene fragment within the second sample set or gene set; and

comparing the mean expression levels for the two sample sets or gene sets to quantify a change in expression for differentially expressed genes between pairs of DNA fragments.

7. *(Currently amended)* The method of claim 1, ~~wherein the analysis comprises further comprising~~ an E Northern analysis that identifies DNA fragments with regard to a pair of user-selected percentiles over the values for a sample.

8. *(Currently amended)* A computer system comprising:  
 a data warehouse ~~which~~ that comprises three distinct databases comprising a gene expression database for storing quantitative gene expression measurements obtained from microarray samples prepared from ~~for~~ tissues and cell lines~~[[;]],~~ a clinical database for storing sample data on bio-samples and donors ~~corresponding to~~ from which the tissues and cell lines were obtained~~[[;]],~~ and a fragment index database for storing information on biological properties and gene sequences for DNA fragments ~~corresponding to the tissues and cell lines on microarrays from which the gene expression measurements were obtained,~~ wherein the data warehouse is arranged in a relational format;

a staging database for linking gene expression measurements in the gene expression database with sample data in the clinical database and information in the fragment index database;

a data explorer for accessing and analyzing data in the data warehouse; and  
 a user interface in communication with the data explorer for entering a first query, wherein the first query comprises a first sample set or gene set for which additional information is sought, and wherein the sample set comprises a plurality of samples having one or more

selected attributes and the gene set comprises at least one gene having one or more selected properties, and for displaying the results of a correlation of the gene expression measurements with the first sample set or gene set.

9. (*Original*) The computer of claim 8, wherein the data warehouse is constructed in a star relational schema.

10. (*Original*) The computer of claim 8, wherein the data warehouse is constructed in a snowflake relational schema.

11. (*Currently amended*) The computer of claim 8, wherein the data explorer performs a gene signature analysis comprising analyzing the correlated gene expression measurements to identify a present set of DNA fragments that are ~~consistently expressed~~ present within the first sample set or gene set, and an absent set of DNA fragments that are ~~consistently not expressed~~ absent within the first sample set or gene set.

12. (*Currently amended*) The computer of claim 11, wherein the data explorer performs a gene signature differential analysis comprising:

performing a gene signature analysis for a second sample set or gene set;

comparing the two different gene signature analysis results; and

identifying four sets of DNA gene fragments comprising:

a present/absent gene set including fragments that are ~~consistently expressed~~ present within the first sample set or gene set and ~~consistently not expressed~~ absent within the second sample set or gene set;

a present/present gene set including fragments that are ~~consistently expressed~~ present within both the first and second sample set or gene set;

an absent/absent gene set including fragments that are ~~consistently not expressed~~ absent within both the first and second sample set or gene set; and

an absent/present set including fragments that are ~~consistently not expressed~~  
~~absent~~ within the first sample set or gene set and are ~~consistently expressed~~ present  
 within the second sample set or gene set.

13. (*Previously presented*) The computer of claim 8, wherein the data explorer performs a fold change analysis, comprising:

calculating mean expression levels for each gene fragment within the first sample set or gene set;

before or after calculating mean expression levels for the first sample set or gene set, correlating gene expression measurements with a second query comprising a second sample set or gene set;

calculating mean expression levels of each gene fragment within the second sample set or gene set; and

comparing the mean expression levels for the two sample sets or gene sets to quantify a change in expression for differentially expressed genes between pairs of DNA fragments.

14. (*Previously presented*) The computer of claim 8, wherein the data explorer performs an E Northern analysis that identifies DNA fragments with regard to a pair of user-selected percentiles over the values for a sample.

15. (*Currently amended*) A computer program product comprising a computer-usable medium having computer-readable program code embodied thereon relating to a data warehouse comprising gene expression data and related information, the computer program product comprising computer-readable program code for effecting the following steps within a computing system:

arranging the data warehouse into three distinct databases comprising a gene expression database for storing quantitative gene expression measurements ~~for~~ taken from microarray samples prepared from tissues and cell lines, a clinical database for storing sample data on bio-samples and donors ~~corresponding to~~ from which the tissues and cell lines were obtained[[;]], and a fragment index database for storing information on biological properties and gene

sequences for DNA fragments ~~corresponding to the tissues and cell lines~~ on microarrays from which the gene expression measurements were obtained, wherein the data warehouse is arranged in a relational format;

providing a staging database for linking gene expression measurements in the gene expression database with sample data in the clinical database and information in the fragment index database;

providing a user interface for entry of a first query, wherein the first query comprises a first sample set or gene set for which additional information is sought, and wherein the sample set comprises a plurality of samples having one or more selected attributes and the gene set comprises at least one gene having one or more selected properties;

correlating gene expression measurements within the gene expression database with the sample set or gene set of the first query; and

displaying at the user interface the correlated gene expression measurements that are responsive to the first query.

16. *(Original)* The computer program product of claim 15, wherein the data warehouse is constructed in a star relational schema.

17. *(Original)* The computer program product of claim 15, wherein the data warehouse is constructed in a snowflake relational schema.

18. *(Currently amended)* The computer program product of claim 15, further comprising computer-readable program code for effecting a gene signature analysis comprising analyzing the correlated gene expression measurements to identify a present set of DNA fragments that are ~~consistently expressed~~ present within the first sample set or gene set, and an absent set of DNA fragments that are ~~consistently not expressed~~ absent within the first sample set or gene set.

19. *(Currently amended)* The computer program product of claim 18, further comprising computer-readable program code for effecting a gene signature differential analysis and the method further comprises:

performing a gene signature analysis for a second sample set or gene set;  
comparing the two different gene signature analysis results; and  
identifying four sets of DNA gene fragments comprising:

a present/absent gene set including fragments that are ~~consistently expressed~~  
present within the first sample set or gene set and ~~consistently not expressed~~ absent  
within the second sample set or gene set;

a present/present gene set including fragments that are ~~consistently expressed~~  
present within both the first and second sample set or gene set;

an absent/absent gene set including fragments that are ~~consistently not expressed~~  
absent within both the first and second sample set or gene set; and

an absent/present gene set including fragments that are ~~consistently not expressed~~  
absent within the first sample set or gene set and are ~~consistently expressed~~ present  
within the second sample set or gene set.

20. *(Previously presented)* The computer program product of claim 15, further  
comprising computer-readable program code for effecting a fold change analysis comprising:

calculating mean expression levels for each gene fragment within the first sample set or  
gene set;

before or after calculating mean expression levels for the first sample set or gene set,  
correlating gene expression measurements with a second query comprising a second sample set  
or gene set;

calculating mean expression levels of each gene fragment within the second sample set or  
gene set; and

comparing the mean expression levels for the two sample sets or gene sets to quantify a  
change in expression for differentially expressed genes between pairs of DNA fragments.

21. *(Previously presented)* The method of claim 15, further comprising computer-  
readable program code for effecting an E Northern analysis that identifies DNA fragments with  
regard to a pair of user-selected percentiles over the values for a sample.